

Aspergillus Genomes and the Aspergillus Cloud

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ABSTRACT

Aspergillus Genomes is a public resource for viewing annotated genes predicted by various *Aspergillus* sequencing projects. It has arisen from the union of two significant resources: the *Aspergillus*/Aspergillosis website and the Central *Aspergillus* Data REpository (CADRE). The former has primarily served the medical community, providing information about *Aspergillus* and associated diseases to medics, patients and scientists; the latter has focused on the fungal genomic community, providing a central repository for sequences and annotation extracted from *Aspergillus* Genomes. By merging these databases, genomes benefit from extensive cross-linking with medical information to create a unique resource, spanning genomics and clinical aspects of the genus. *Aspergillus Genomes* is accessible from <http://www.aspergillus-genomes.org.uk>.

INTRODUCTION

An important consequence of the impact of global climate change, brought to the fore by recent natural disasters, has been a stimulation of interest in fungal ecology. In the aftermath of Hurricanes Katrina and Rita, for example, residential areas in New Orleans, having remained underwater for weeks, succumbed to rapid mould growth (1–3), facing residents with significant health hazards: exposure to high concentrations of some moulds (e.g. *Aspergillus*, *Cladosporium* and *Trichoderma*) can cause severe and sometimes life-threatening responses. Examination of samples taken from affected homes identified several *Aspergillus* species, *Aspergillus niger* being predominant amongst them. The concentration of this and other species reached levels generally associated with environmental health problems. The paucity of effective drugs available to treat *Aspergillus* infections, coupled with the speed of

diagnosis required for successful treatment, raises concerns for residents and tradesmen who return to restore such areas without taking appropriate protective measures.

Generally, *Aspergillus* is a genus of fungus found worldwide: approximately 250 species descriptions have been published (4,5), several of which are of medical or industrial importance. *Aspergillus fumigatus* is the most common mould pathogen of humans, causing both life-threatening invasive disease of immuno-compromised patients and allergic disease in patients with atopic immune systems (6–8). *Aspergillus nidulans*, an occasional human pathogen, is a model organism that has contributed to our understanding of genetics, gene regulation and cellular biology (9,10), while *A. niger* (11,12) and *A. oryzae* (13) are both used in industrial processes. *Aspergillus flavus* is both a human and plant pathogen, being responsible for a disproportionate number of cutaneous and wound infections in man (14). Several other *Aspergillus* species are known to be significant allergens or to be responsible for mycotoxin production in stored food (15–17).

In light of their relevance to medicine and industry, and the desire to better understand this genus, the genomes of 10 *Aspergilli* have recently been sequenced, seven of which have been annotated in worldwide collaborative efforts. To be of maximum benefit to the community in general, this expanding pool of genomic data (the volume of which is likely to increase with the decreasing cost of sequencing) requires collation and long-term maintenance; more particularly, to benefit research into Aspergillosis and other illnesses caused by this genus, the accumulating genomic data needs to be cross-linked to the numerous *Aspergillus*-related medical reports now available. However, the standard model for genome databases [e.g. SGD (18)] is not appropriate for medically significant organisms, where the dissemination of information, such as patient care, drug resistance or toxins is equally important. Thus, *Aspergillus Genomes* was established in April 2008 to provide links between genomic and medical information and to provide access through one portal.

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SOURCE DATA AND METHODS

This resource is a joint undertaking by two teams that have, until now, provided online medical and genomic information for different groups within the *Aspergillus* community.

Medical information

The *Aspergillus/Aspergillosis* website (<http://www.aspergillus.org.uk>) was designed to serve the medical and translational research communities, including medical consultants, scientists, patients and their relatives. Offering a wealth of information about *Aspergillus* and the multiple diseases (known collectively as Aspergillosis) it can cause, one section provides advice and a discussion group for patients, while other areas provide medical and species images, educational materials, meeting reports and publications. As part of Aspergillus Genomes, this large collection of material offers a valuable repository from which we can begin to derive much-needed medical insights from genome analyses (Some sections require registration, please refer to supplement 'Note: Access information').

Genomic information

The Central *Aspergillus* Data REpository, CADRE (<http://www.cadre-genomes.org.uk>) (19), was developed primarily to serve the *Aspergillus* genomics community. Its principal role has been to manage genomic data and to offer web-based tools for analysis and visualization of genomic features. These tools offer simple displays for viewing annotation of predicted genes (e.g. function, GO terms, similarity matches) and of their protein products (e.g. family and domain similarity matches), as well as complex displays for viewing genes and other features (e.g. RNA-encoding genes, repeated sequences) in the context of an assembly.

Incorporation of this resource into Aspergillus Genomes provides access to seven annotated genomes, five of which are of particular importance to the *Aspergillus* genetics community (*A. fumigatus* Af293 and A1163, *A. nidulans*, *A. oryzae* and *A. niger*); of these, two are clinical isolates (*A. fumigatus* Af293 and A1163).

CONTENT OF CURRENT RELEASE

Aspergillus Genomes has been implemented using Ensembl version 22 (20), a suite devised for storing annotated eukaryotic genomes. The latest release (June 2008) contains information pertaining to seven genomes.

Aspergillus fumigatus (Af293) 2.2.1

Using whole-genome shotgun (WGS) sequencing (carried out by TIGR) and optical mapping, this project yielded an assembly of 19 supercontigs (~28.8 Mb) mapping onto eight chromosomes. Using automated gene predictions, the University of Manchester coordinated an international manual annotation project, and data for 9926 genes were released in 2005 (21). This genome has since been re-annotated as part of an additional international comparative project led by the J. Craig Venter Institute

(JCVI) and the University of Manchester. Data for 9630 predicted protein-coding genes were publicly released in 2008 (22).

Aspergillus nidulans (FGSC A4) 5.3.1

WGS sequencing of this genome was undertaken by the Broad Institute and publicly released in March 2003. This project yielded an assembly of 17 supercontigs (~30 Mb) assigned to eight linkage groups, a group of unassigned fragments (84 contigs) and 9520 predicted protein-coding genes. Further automated and manual annotation carried out by TIGR (2005) yielded a total of 10 542 genes (23)—using publicly available linkage data (John Clutterbuck, <http://www.gla.ac.uk/ibls/molgen/aspergillus/index.html>) and in-house analyses, we have updated the original Broad assembly to reflect these findings. More contigs have now been mapped, with correct orientation, within each supercontig; the supercontigs have also been orientated correctly within each linkage group.

Aspergillus oryzae (RIB 40) 1.1.1

WGS sequencing of this genome was undertaken by a Japanese Consortium, led by the National Institute of Advanced Industrial Science and Technology (AIST). Using optical mapping, the project yielded an assembly of 22 supercontigs (~37.1 Mb) mapped to eight chromosomes and a group of unassigned fragments. Using automated annotation techniques, 12 074 protein-coding genes were predicted and publicly released in 2005 (24).

Aspergillus niger (CIB 513.88) 1.1.1

Using WGS sequencing and BAC walking (carried out by DSM Food Specialties), this project yielded 19 supercontigs (~33.9 Mb) mapping onto eight chromosomes. Using a base of automated gene predictions, DSM coordinated a European manual annotation project, predicting 14 086 protein-coding genes, and data were released in 2007 (25).

Aspergillus fumigatus (A1163) 1.1.1, *A. clavatus* (NRRL 1) 1.1.1 and *Neosartorya fischeri* (NRRL 181) 1.1.1

These genomes were sequenced using WGS sequencing (carried out by JCVI), as part of an international comparative project led by JCVI and the University of Manchester (2008) (22). The work on *A. fumigatus* yielded 55 scaffolds (~29 Mb), for which 9929 protein-coding genes were predicted; *A. clavatus* yielded 143 unassigned fragments (~27.8 Mb), for which 9121 protein-coding genes were automatically predicted; and *N. fischeri* yielded 976 unassigned fragments (~32.5 Mb), for which 10 406 protein-coding genes were automatically predicted.

DISPLAY AND SEARCH SOFTWARE

Several tools are provided (via CADRE) for viewing genomic data within Aspergillus Genomes. GeneView (Supplementary Figure S1) is the principal data-visualization tool, offering detailed information about a particular gene, including the public locus, the chromosomal location and a short description of the gene. An overview of each predicted transcript is also provided: this consists of

structure information, a list of database cross-references to similar sequences (e.g. SGD) and protein features [e.g. InterPro (26)], and GO terms that have been mapped to the gene. Images are also displayed of each transcript structure and of domains or family signatures mapped to the protein.

In addition to the information provided in GeneView, Transview provides the transcript sequence, which can be marked up to highlight both codons and the peptide sequence. ExonView provides the nucleotide sequence for each exon, as well as the upstream and downstream regions, untranslated regions and introns. ProtView displays further information about a particular protein and, in addition to the GeneView summary it provides the sequence in FASTA format, which can be marked up to highlight exons. ProtView also provides some predicted peptide statistics and information about any matches to family- or domain-based databases [e.g. Pfam (27), PRINTS (28)].

Four search tools, all accessible from the homepage, are available for Aspergillus Genomes: UniSearch, GoogleTM customized search, the Aspergillus Cloud and BLAST. UniSearch, the in-built Ensembl search tool, allows users to search public identifiers assigned to genes (e.g. AFUB_063690 and An14g07380)—it is found on the homepage and throughout the website. A familiar tool is provided in the form of a customized GoogleTM search engine, thus enabling free-text searches on all information pages and genomes within the resource. A more recent addition is ‘cloud’ searching, which is described in more detail below. To allow similarity searches, BLAST can be performed against in-house sequences (i.e. genomic sequence, predicted ORFs and proteins), the results of which are presented in the context of the assembly rather than as stand-alone alignments.

THE ASPERGILLUS CLOUD

The results of UniSearch or GoogleTM searches are provided in the form of lists of pages and documents matching the given term. Although useful in many cases, this type of output does not empower the user to access and search related data. To remedy this, we have introduced the Aspergillus Cloud, a facility that uses ‘cloud’ searching (developed by QuinturaTM) across the medical and genomic information embraced by Aspergillus Genomes. Cloud searching provides a visual means of searching related terms: when a search term is entered, this generates a group (or cloud) of related terms from context, as well as a list of hyperlinks to relevant pages/documents. Furthermore, by exploring the cloud (i.e. by moving a mouse over any term), search results change to reflect relationships with the new highlighted term.

We can demonstrate the Aspergillus Cloud using documented research on point mutations in the cyp51a gene and its correlation to rising triazole drug resistance. By simply entering ‘cyp51a’ into the search box (Figure 1), a number of related terms are displayed, as well as a number of hyperlinks to relevant pages. Several links provide access to pages that are contained within the medical

section of Aspergillus Genomes and refer to point mutations within the gene and drug resistance; one provides access to the relevant gene within the genomic section of Aspergillus Genomes. Medical terms can also be used to explore the Aspergillus Cloud (Figure 2). By entering the term ‘Allergic Bronchopulmonary Aspergillosis’ (ABPA; an allergic reaction to *Aspergillus* spores), opportunities are given to explore articles written about the allergen to which ABPA patients are hypersensitive, as well as annotation provided for an ABPA-related gene.

The Aspergillus Cloud provides a powerful means of exploring Aspergillus data and finding medical reports linked to particular genes that would require several search attempts or would otherwise be missed using conventional search tools.

EXPLORING FEATURES OF INTEREST

The collation of *Aspergillus* data enables us to focus on and embellish features of medical interest. *Aspergillus fumigatus*, for example, possesses over 80 genes encoding allergen proteins and of these 22 have been cloned as IgE binding (29,30). We have documented these allergens within Aspergillus Genomes and provided links to annotated genes (http://www.aspergillus.org.uk/indexhome.htm?secure/sequence_info/genesofinterest/allergens.php). Another area of great interest is secondary metabolites. We have already extracted information on many secondary metabolites (http://www.aspergillus.org.uk/secure/metabolites/list_by_secmet.php) and intend to link this data to annotated genes. We also have begun the process of highlighting secondary metabolite clusters, such as the gliotoxin biosynthetic cluster. Gliotoxin is a toxin produced by *A. fumigatus* and possesses many biological properties, including the ability to act as an antibacterial and antiviral agent as well as an immunosuppressant (31,32). We have provided a view of the gene cluster within the assembly and links to the appropriate annotation (Figure 3).

FUTURE DIRECTIONS

In the short term, we plan to add three more new genomes and to revise a fourth. The new genomes include *A. flavus* NRRL 3357 (TIGR, 2005), *A. terreus* (Broad Institute, 2006) and *A. niger* ATCC 1015 (DOE Joint Genome Institute, 2006); although these genomes have been sequenced with high coverage, only draft sequence and limited annotation are currently publicly available—we will add the sequence data to our collection for comparative work and add annotation as it becomes available. As for the latter, we are currently participating in Eurofungbase, a European project coordinated by Eurofung (<http://www.eurofung.net>), to manually re-annotate *A. nidulans* with the help of experts from 32 laboratories and 13 industrial partners. Our role is to house the corrected gene structures and annotation arising from this project, and to make the data publicly available: we are processing this information in-house, and will release it through CADRE and Aspergillus Genomes.

(a)

The Aspergillus Cloud search results for 'cyp51a' show a tree diagram and a list of documents.

- Tree Diagram:**
 - Root: cyp51a
 - Level 1: mutation, fumigatus, combination, sterol, alpha, alteration
 - Level 2: mutation leads to 'Aspergillus website articles' (1-5)
 - Level 2: fumigatus leads to 'Aspergillus website articles' (1-5)
 - Level 2: combination leads to 'Aspergillus website articles' (1-5)
 - Level 2: sterol leads to 'Aspergillus website articles' (1-5)
 - Level 2: alpha leads to 'Aspergillus website articles' (1-5)
 - Level 2: alteration leads to 'Aspergillus website articles' (1-5)
 - Level 3: 'Aspergillus website articles' (1-5) lead to detailed document snippets.
- Document List:**
 1. Aspergillus website articles: A new Aspergillus fumigatus resistance mechanism conferring in vitro cross-resistance to azole antifungals involves a combination of Cyp51a alterations. http://www.aspergillus.org.uk.../allRows_Recordset1=1425
 2. Aspergillus website articles: Differences in interactions between azole drugs related to modifications in the 14-alpha sterol demethylase gene (Cyp51a) of Aspergillus fumigatus. http://www.aspergillus.org.uk.../allRows_Recordset1=1442
 3. Aspergillus website articles: Total resistance diversity of the 14-alpha sterol demethylase (Cyp51a) in Aspergillus fumigatus and its role in azole drug susceptibility. http://www.aspergillus.org.uk.../allRows_Recordset1=1424
 4. Aspergillus website articles: Rapid, High-Throughput, Multiplex, Real-time PCR for Identification of Mutations in the Cyp51a Gene of Aspergillus fumigatus That Confer Resistance to Itraconazole. http://www.aspergillus.org.uk.../allRows_Recordset1=1425
 5. Ensembl Aspergillus fumigatus (geneweb): Locus, 14-alpha sterol demethylase Cyp51a, identical to 14-alpha sterol demethylase (GI:14861413) (Aspergillus fumigatus) PMID: 11427550, (1.14.13.) http://www.ncbi.nlm.nih.gov/gene/AFUA_4G06890

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(b)

Record number 391 out of a total of 1442 in this database.

Title: Differences in interactions between azole drugs related to modifications in the 14-alpha sterol demethylase gene (Cyp51A) of Aspergillus fumigatus.

Author: Garcia-Effron G, Mellado E, Gomez-Lopez A, Alcazar-Fuoli L, Cuena-Estrella M, Rodriguez-Tudela JM

Date added to website: 2005-06-07

Detail: ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, May 2005, p. 2119–2121 Vol. 49, No. 5

Abstract: The combined activity of different azole drugs was investigated. Thirty-one Aspergillus fumigatus strains were tested, including two cyp51A^{-/-} and one cyp18C^{-/-} gene-knockout strain andazole-susceptible and -resistant strains with different resistance mechanisms. The combination of itraconazole and voriconazole was synergistic for all strains except for those with gene knockouts.

Go to article

(c)

Gene Report

Gene ID: AFUA_4G06890

Genomic Location: View gene in genomic location: 2141884 – 2143502 bp (2.1 Mb) on supercontig 96. This gene is located in sequence: An03c0032

Description: At4g06890 (Alt. Locus), 14-alpha sterol demethylase Cyp51A, identical to 14-alpha sterol demethylase (GI:14861413) (Aspergillus fumigatus) PMID: 11427550, (1.14.13.)

Prediction Method: First-pass computational and manual annotation were carried out via TIGR and the Wellcome Trust Sanger Institute via TIGR and the Wellcome Trust Sanger Institute. Subsequent annotation was performed by a European consortium led by DSM Food Specialties. i.e., NAP, BLASTP, InterProScan, HMM2, Prosite, SignalP and TMHMM. Secondary computational and manual annotation were carried out via the JCVI as part of an international comparative project in 2007.

Prediction Transcript: AFUA_4G06890 [Transcript information] [Exon information] [Protein information]

Transcript Neighbourhood: A diagram showing the genomic neighborhood of the gene.

Export Data: Export gene data in EMBL, GenBank or FASTA

(a)

The Aspergillus Cloud search results for 'allergic bronchopulmonary aspergillosis' show a tree diagram and a list of documents.

- Tree Diagram:**
 - Root: allergic bronchopulmonary aspergillosis
 - Level 1: lung, sinusitis, patient, stable, bronchopulmonary aspergillosis, asthma, lesson
 - Level 2: lung leads to 'allergen' (highlighted with a red oval)
 - Level 2: sinusitis leads to 'allergen' (highlighted with a red oval)
 - Level 2: patient leads to 'allergen' (highlighted with a red oval)
 - Level 2: stable leads to 'allergen'
 - Level 2: bronchopulmonary aspergillosis leads to 'allergen'
 - Level 2: asthma leads to 'allergen'
 - Level 2: lesson leads to 'allergen'
 - Level 3: 'allergen' leads to 'Aspergillus website articles' (1-5)
- Document List:**
 1. Aspergillosis: Allergic bronchopulmonary aspergillosis (ABPA) - normal and infected. <http://www.aspergillus.org.uk/aspergillosis.htm>
 2. Aspergillosis: Allergic bronchopulmonary aspergillosis. <http://www.aspergillus.org.uk/abpa.htm>
 3. Allergic bronchopulmonary aspergillosis: Allergic bronchopulmonary aspergillosis (ABPA) - normal and infected. <http://www.aspergillus.org.uk/asfa.htm>
 4. Avian Aspergillosis References: KNUTSEN, A. P. MUELLER, K. M. HUTCHISON, P. S and SLOANE, R. D. Allergic serum anti-Aspergillus fumigatus antibodies by immunoassay and ELISA in cystic fibrosis with allergic bronchopulmonary aspergillosis. http://www.aspergillus.org.uk.../view?genie=AFUA_4G06890
 5. The Aspergillus/Aspergillosis Website: ABPA and aspergillosis. Some asthma patients with very severe asthma may also be sensitised to fungi like aspergillus (SADS). There is a section dedicated to the needs of patients. <http://www.aspergillus.org.uk/asfa.htm>

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(b)

Aspergillus/Aspergillosis Articles search

Background: Patients with cystic fibrosis (CF) can become colonized with aspergillus, which can act as an allergen and/or as an allergic bronchopulmonary aspergillosis (ABPA) (ABPA).

2. Aspergillosis: ... allergic bronchopulmonary aspergillosis allergen Rasp f4 from patient Wof028624-A1 - Aspergillus fumigatus homologous protein of Aspergillus fumigatus homolog Rasp f4 is a non-secreted protein of unknown function and is related to allergic bronchopulmonary aspergillosis (ABPA) in human. http://www.ncbi.nlm.nih.gov/gene/AFUA_4G06890

3. Aspergillosis: Potential role of the cellular allergen stimulation test (CAST) in diagnosis of allergic bronchopulmonary aspergillosis (ABPA) in cystic fibrosis http://www.ncbi.nlm.nih.gov/gene/AFUA_4G06890

4. Aspergillus website article: Asp f6, an Aspergillus allergen specifically recognized by IgE from patients with allergic bronchopulmonary aspergillosis, is differentially expressed during germination. http://www.ncbi.nlm.nih.gov/gene/AFUA_4G06890

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(c)

Gene Report

Gene ID: An03g00770

Genomic Location: View gene in genomic location: 30060 – 31181 bp (30.1 Kb) on config An03c0030. This gene is located in sequence: An03c0030

Description: Title: strong similarity to hypothetical allergic bronchopulmonary aspergillosis allergen fAsp f4 from patent WO028624-A1 - Aspergillus fumigatus; The Aspergillus fumigatus homolog fAsp f4 is a non-secreted protein of unknown function and is related to allergic bronchopulmonary aspergillosis (ABPA) in human. First-pass computational annotation was carried out by a European consortium led by DSM Food Specialties. ORFs were chiefly predicted using FGENESH. PEDANT-ProTm was used to analyse each ORF, for which predicted features were manually verified and annotated.

Prediction Method: 1: An03g00770 [Transcript information] [Exon information] [Protein information]

Prediction Transcript: An03g00770 [Transcript information] [Exon information] [Protein information]

Transcript Neighbourhood: A diagram showing the genomic neighborhood of the gene.

Export Data: Export gene data in EMBL, GenBank or FASTA

(d)

Record number 594 out of a total of 1436 in this database.

Title: Asp f6, an Aspergillus allergen specifically recognized by IgE from patients with allergic bronchopulmonary aspergillosis, is differentially expressed during germination.

Author: Schweihsbacher M, Israel L, Heesemann J, Ebel F.

Date added to website: 2006-04-18

Detail: Aspergillus fumigatus is a pathogenic mould causing allergic and invasive respiratory diseases. Allergic bronchopulmonary Aspergillosis (ABPA) is a severe pulmonary complication resulting from hypersensitivity to A. fumigatus proteins. Aspergillus allergen Asp f6 is recognized by IgE from ABPA patients, but not from sensitized individuals in the general population. Two different bands were found in two groups of allergic patients. METHODS: Proteins from hyphae, resting and germinating conidia of A. fumigatus were compared by SDS-PAGE. Protein identification was performed using MALDI-TOF mass spectrometry. Recombinant

Abstract: Go to article

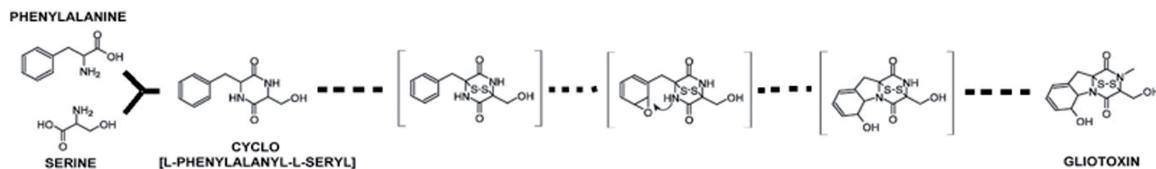
First/Previous/ Next/Last

Go to articles section of Aspergillus Website

Figure 2. Using the Aspergillus Cloud to explore medical information. Entering a medical condition, such as ABPA, into the search box (a), produces several groups of related terms within the search space below. By moving the mouse over each term, new clouds arise temporarily. Clicking on a term will add the associated clouds into the search space and change the focus of the search to include the term (b). In this example, we find a list of documents on the RHS that includes links to an ABPA-related gene (c) and to an article regarding an allergen that is particular to the allergic response of ABPA patients (d).

Cluster 27. Gliotoxin biosynthetic cluster.

Gliotoxin is regarded as one of the most important toxins produced by *A. fumigatus*. You can link to the secondary metabolites and toxins page [here](#) for more information on this compound.



Gliotoxin is synthesised from the amino acids phenylalanine and serine by a nonribosomal peptide synthetase GliP. The resulting L-phenylalanyl-L-seryl compound then appears to undergo a series of oxidative enzymatic transformations before conversion to mature gliotoxin by a methylation step. Evidence for this reaction pathway is limited but comparison with sirodesmin biosynthesis in *Leptosphaeria maculans* has provided valuable insights. (Cramer RA et al. Disruption of a Nonribosomal Peptide Synthetase in *Aspergillus fumigatus* Eliminates Gliotoxin Production. *Eukaryot Cell*. 2006; 5(6): 972-980, Gardiner and Howlett, Bioinformatic and expression analysis of the putative gliotoxin biosynthetic gene cluster of *Aspergillus fumigatus* FEMS Micro Lett 2006; 248:241-248)

Cluster 27 information:



Cluster 27 map. Click on the image to go to an active cluster 27 map with links to genes in the database.

Cluster 27 details									
Species	Gene ID	Start position	End position	Chromosome	Strand	Function	Gene status	Protein status	Associated genes
<i>A. fumigatus</i>	AFIA_00001	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00002	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00003	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00004	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00005	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00006	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00007	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00008	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00009	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00010	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00011	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00012	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00013	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00014	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00015	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00016	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00017	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00018	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00019	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00020	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00021	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00022	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00023	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00024	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00025	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00026	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00027	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00028	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00029	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00030	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00031	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00032	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00033	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00034	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00035	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00036	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00037	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00038	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00039	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00040	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00041	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00042	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00043	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00044	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00045	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00046	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00047	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00048	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00049	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00050	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00051	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00052	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00053	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00054	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00055	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00056	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00057	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00058	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00059	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00060	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00061	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00062	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00063	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00064	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00065	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00066	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00067	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00068	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00069	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00070	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00071	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00072	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00073	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00074	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00075	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00076	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00077	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00078	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00079	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00080	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00081	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00082	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00083	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00084	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00085	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00086	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00087	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00088	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00089	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00090	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00091	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00092	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00093	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00094	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00095	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00096	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00097	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00098	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00099	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00100	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00101	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00102	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00103	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00104	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00105	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00106	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00107	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00108	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00109	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00110	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00111	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00112	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00113	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00114	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00115	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00116	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00117	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00118	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00119	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00120	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00121	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00122	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00123	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00124	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00125	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00126	0	200	1	-	Unknown	Active	Unknown	Unknown
<i>A. fumigatus</i>	AFIA_00127	0	200</td						

Conflict of interest statement: None declared.

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